

FIGURE 1
Map of a First IL-17 Receptor Like cDNA (SEO ID No: 1)
and Amino Acid (SEO ID NO: 2)

1 ATAAAAGCGCAGCGTGC GGCTGGCTGGATCCCGCGCAGTGCGCCGCGCATGTCGCTCGT 60
M S L V -

61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCGAGAGCCGACCGTTCAATG 120
L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACATAGTGTGCAACAGGGGACTATTCAAT 240
L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300
L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGCTGTGTGAGGTGCAATTA 360
K I C V T G K S N F Q S Y S C V R C N Y -

361 CACAGAGGCCCTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTTCTACAT 420
T E A F Q T Q T R P S G G K W T F T S Y I -

421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCAATATTCTTAATGC 480
G F P V E L N T V Y F I G A H N I P N A -

481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540
N M N E D G P S M S V N F T S P G C T L D -

541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACAT 600
H I M K Y K K K C V K A G S L W D P N I -

601 CACTGCTTGTGAAGAAGATGAGGAGACAGTAGAAGTGAACCTCACAAACCACTCCCTTGGG 660
T A C K K N E E T V E V N F T T T P L G -

661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTGA 720
N R Y M A L I Q H S T I I G F S Q V F E -

721 GCCACACCGAAGAAACAAACGCGAGCTTCAGTGGTGATTCAGTGACTGGGGATAGTGA 780
P H Q K K Q T R A S V I P V T G D S E -

781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840
G A T V Q L T P Y F P T C G S D C I R H -

841 TAAAGGAACAGTTGTGCTCTGCCCAAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900
K G T V V L C P Q T G V P F P L D N N K -

901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCTCTGCTGTCTGCTGCTGGTGGCCACATGGGT 960
S K P G G W L P L L L L S L L V A T W V -

961 GCTGGTGCGAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020
L V I Y Y L M W R H E I K K T L D N K -

1021 TACCACCACACTACTGCCCCCATTAAAGTTCCTGTGGTTTACCCATCTGAAATATGTTT 1080
T T T L L P P I K V L V V Y P S E I C F -

1081 CCATACACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAATGCAGAAGTGAGGTCAT 1140
H H T I G C Y F T E F L Q N H C R S E V I -

1141 CCTCGAAAAGTGCGAAAAAGAAATAGCAGAGATGGGTCCAGTGAGTGCTTGGCCAC 1200
L E K W Q K K K I A E M G P V Q W L A T -

Figure 1 (continued)

1201 TCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTG 1260
Q K K A A D K V V F L L S N D V N S V C -

1261 CGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCC 1320
D G T C G K S E G S P S E N S Q D L F P -

1321 CCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCACTGTCACAAATACGT 1440
L A F N L F C S D L R S Q I H L H K Y V -

1441 GGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCC 1500
V V Y F R E I D T K D D Y N A L S V C P -

1501 CAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCA 1560
K Y H L M K D A T A F C A E L L H V K Q -

1561 GCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCC 1620
Q V S A G K R S Q A C H D G C C S L *

1621 CACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAaaaaac 1680

1681 GTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAAACATT 1740

1741 TATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAC 1800

1801 TACATTTACAACCTTCAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAA 1860

1861 CTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCAGC 1901

10520-22002

FIGURE 3
Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4)
And Amino Acid (SEQ ID NO: 5) Sequences

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1 ATAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCGCGATGTCGCTCGT 60
                                     M S L V -
61 GCTGCTAAGCGTGGCCGCGCTGTGCAGGAGCGCGTACCCGAGAGCCGACCGTTCAATG 120
   L L S L A A L C R S A V P R E P T V Q C -
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
   G S E T G P S P E W M L Q H D L I P G D -
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCAAT 240
   L R D L R V E P V T T S V A T G D Y S I -
241 TTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300
   L M N V S W V L R A D A S I R L L K A T -
301 CAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCAGCTGTGTGAGGCTGGAGTG 360
   K I C V T G K S N F Q S Y S C V R L E C -
361 CAGTGGTGCAGTATGGCTCGCTGCGACCTCAATCTTCTGGGCTCAAGCGATCGTTCTGC 420
   S G A I M A R C D L N L G S S D R S A -
421 TTCAGCTCCCGAGCGCTGGGACTGCAGGCGTGGGCCACCAGACCTGGCTAATTTTTGT 480
   S A S R A A G T A G V G H Q T W L I F V -
481 AGTTTTTTGTAGAGGGGGTTTCCCGTGTGTGCTGCTTGAATTCAGTGCTCAGGCGAT 540
   V F V E G G F T V L L V L N S S A Q A I -
541 CTGCCTGCCTCGGCTTCCCAAAGTGCTGGGATTACAGTGGACATTTTCCATACATCGGCTT 600
   C L P R L P K V L G L Q W T F S Y I G F -
601 CCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAATAT 660
   P V E L N T V Y F I G A H N I P N A N M -
661 GAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGTGCTAGACCACAT 720
   N E D G P S M S V N F T S P G C L D H I -
721 AATGAAATATAAAAAAGTGTGCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGC 780
   M K Y K K K C V K A G S L W D P N I T A -
781 TTGTAAGAAGATGAGGAGACAGTAGAAGTGAACCTTCAACCACTCCCGTGGGAAACAG 840
   C K K N E E T V E V N F T T T P L G N R -
841 ATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTAGGCCACA 900
   Y M A L I Q H S T I I G F S Q V F E P H -
901 CCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGTGC 960
   Q K K Q T R A S V V I P V T G D S E G A -
961 TACGGTGCGAGTGA CTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGG 1020
   T V Q L T P Y F P T C G S D C I R H K G -

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CGCGGCTGCTGCTCGT

Figure 3 (continued)

1021 AACAGTTGTGCTCTGCCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAA 1080
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT 1140
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGATCTATCTAATGTGGAGGCAGAAAGGATCAAGAAGACTTCCTTTTCTACCAC 1200
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACTGCCCCCCATTAAAGTTCTTGTGGTTTACCCTCTGAAATATGTTTCCATCA 1260
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTATCCTCGA 1320
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAAGTGGCTTGCCACTCAAAA 1380
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCAACAGTGTGTGCGATGG 1440
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAGCTCTCAAGACCTCTTCCCCCTTGC 1500
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCTTTTCTGCAAGTATCTAAGAAGCCAGATTATCTGCACAAATACGTGGTGGT 1560
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTA 1620
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGT 1680
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGTCTGCTCCTTGTAGCCCCACCA 1740
S A G K R S Q A C H D G C C S L *

1741 TGAGAAGCAAGAGACCTTAAAGGCTTCTATCCACCAATTACAGGAAAAAACGTGTGA 1800

1801 TGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAACAATTTTATACC 1860

1861 AATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGAAAACATACATT 1920

1921 TACAACCTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACGTAA 1980

1981 CCATTTTGATAATGCAACAATAAAGCATCTTCAGC 2015

FIGURE 4
Homology of a Second IL-17 Human Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID NO: 5) and KNOWN Human IL 17
Receptor Family Member (SEQ ID NO: 3).

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1 MSLVLLSLAALCRSAVPREPTVQCGETGPSPEWMLQHDLPGLDRDLRV 50
1 .....:MGAARS 6
51 EPVTTSVATGDYSILMNVSVWLR.ADASIRLL.KATKICVTGKSNFQSYS 98
7 PP..SAVPGPLLGLLLLLLGLVLA PGGASRLLLDHRALVCSQPGLNCTVK 54
99 CVRLCSCGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
55 STCLDSW.IHPR...NLTPSSPKDLQIQHFAHTQQGDLFPVAHIEWTL 100
143 ...FVVFVEGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
101 QTDASILYLEGAELSVLQLNTN.ERLCVRFELSKLRHHHRRWRFTFSHF 149
185 PVELNTVYFIGAHNIPNANMNEDGPSMSVNF TSPGCLDHIMKYKKKCVKA 234
150 VVDPDQYEYEVTVHHLKPKIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235 GSLWDPNITACKNEETVEVNF TTP LGNRYMALI.....QHSTIIGF 277
200 GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHM 249
278 SQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYVPTCGSDCIRHKG 324
250 HHIPAPRPEEFHQRSNVTLT LRLNKGCCR HQVQIQPFSSCLNDCLRHSA 299
325 TVVLC PQ.TGVFPFLDNNKS KPGGWLPLLLLSLLVATWVLVAGIYLMWRH 373
300 T.VSCPMPDTPPEPIPDYMP LWVYWF.ITGISILLVGSVILLIVCMTWRL 347
374 ERIKKTFSFTTT.....LLP....PIKVLVVPYSE.ICFHHTICY 408
348 AGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVLK 397
409 FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATOK...KAADKVVFLL 454
398 FAQFLLTACGTEVALDLLEEQAISEAGVMTWVG RQKQEMVESNSKIIVLC 447
455 SNDVNSVDCGTGCGKSEGPS.....SENSQDLFLPLAFNLFCSDLRSQIH 497
448 SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDKRPAC 495
498 LHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQV 544
496 FGTYYVVCYFSEVSCDGDVDPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPG 545
545 SAGKRSQACHDGCSSL*..... 561
546 RMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADD 595

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FIGURE 5
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6)
and Amino Acid (SEQ ID NO: 7) Sequence

1 ATAAAGCGCAGCGTGGGTGGCTGGATCCCGCGCAGTGGCCCGCGATGTCGCTCGT 60
61 GCTGCTAAGCCTGGCCGCTGTGTCAGGAGCGCGTACCCGAGAGCCGACCGTTCAATG 120
121 TGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGAGA 180
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACATAGTGTGCAACAGGGGACTATTCAAT 240
241 TTTGATGAATGTAAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCTACATCGGCTTCC 300
M W T F S Y I G F P -
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAAATGA 360
V E L N T V Y F I G A H N I P N A N M N -
361 ATGAAGATGGCCCTTCCATGTCTGTAATTTCACCTCACCAGGCTGCCTAGACCACATAA 420
E D G P S M S V N F T S P G C L D H I M -
421 TGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACACTACTGCTT 480
K Y K K K C V K A G S L W D P N I T A C -
481 GTAAGAAGATGAGGAGACAGTAGAAGTGAACCTTCAACAACACTCCCTCGGGAACAGAT 540
K K N E E T V E V N F T T P L D H I M -
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTGAAGCCACACC 600
M A L I Q H S T I I G F S Q V F E P H Q -
601 AGAAGAAACAACGCGAGCTTCAGTGGTGATTCCAGTGAAGTGGGGATAGTGAAGGTGCTA 660
K K Q T R A S V V I P V T G D S E G A T -
661 CGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720
V Q L T P Y F P T C G S D C I R H K G T -
721 CAGTTGTGCTCTGCCCAAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAGCAAGC 780
V V L C P Q T G V P F P L D N N K S K P -
781 CGGGAGGCTGGCTCGCTCTCTCTCTGCTGCTGGTGGCCACATGGGTGCTGGTGG 840
G G W L P L L L L S L L V A T W V L V A -
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900
G I Y L M W R H E R I K K T S F S T T T -
901 CACTACTGCCCCCCATTAAAGTTCCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960
L A P P I K V L V V Y P S E I C F H H T -
961 CAATTGTGTACTTCTACTGAATTTCTTCAAACCATTGCAGAAGTGAAGGTCATCCTCGAAA 1020
I C Y F T E F L Q N H C R S E V I L E K -
1021 AGTGGCAGAAAAAGAAATAGCAGAGATGGGTCCAGTGTCAGTGGCTTGGCACTCAAAAAA 1080
W K K K I A E M G P V Q W L A T P Q K A -
1081 AGGCAGCAGACAAAGTCGTCTTCTCTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140
A A D K V V F L L S N D V N S V C D G T -
1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAGTCTCAAGACCTCTTCCCCTTGCCCT 1200
W K S E G S P S E N S Q D L F A T P Q K A -
1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCT 1260
N L F C S D L R S Q I H L H K Y V V V Y -
1261 ACTTTAGAGAGATTGATACAAAAGCAGATTACAATGCTCTCAGTGTCTGCCCAAGTACC 1320
F R E I D T K D D Y N A L S V C P K Y H -

Figure 5 (continued)

1321 ACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGT 1380
L M K D A T A F C A E L L H V K Q Q V S -
1381 CAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCATG 1440
A G K R S Q A C H D G C C S L *
1441 AGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATG 1500
1501 ATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAACATTTTATACCAA 1560
1561 TAAAAATTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTA 1620
1621 CAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACGTGTAACC 1680
1681 ATTTTGATAATGCAACAATAAAGCATCTTCAGC 1713

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```

      1 .....MNTFSYIGFP 10
          |||
101 QTDASILYLEGAELSVLQLNTRNERLCVRFEFLSKLRHHHRRWRFTFSHFV 150
          |||
    11 VELNTVYFIFGAHNIPNANNMEDGPSMSVNFTSPGCLDHIMKYKKKCKVKAG 60
          |||::|||
151 VDPDQEYEVTVHHLPKPIPDGGPNHQSKNFLVPDCEHARKMVTTPCMSSG 200
          |||
    61 SLWDPNITACKNKETEVEVNFNTPPTLGNYMALI.....QHSTIIIGFS 103
          |||||||
201 SLWDPNITVTLEAHQLRVSFTLWNETHYQILLTSPFHMEHNSCFEHMH 250
          |||
   104 QVFEPHQKQTTRASVIPVTGDSEGA...TVOLTYPPTFCGSDCIRHKGT 150
          |||::|||
251 HIPAPRPPEEFHORSNVILTLRNLKGCCRHQVIQFFPSSCLNDCLRHSAT 300
          |||
151 VVLCPQ.TGVPPPLDNNSKPGGWLP LLLLSSLVATWVLVAGIYLMWRHE 199
          |||::|||
301 .VSCPMPDTPPEPIDPYMLPWYWF.ITGISLLVGSVILLIVCMTRLA 348
          |||
200 RIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICYF 234
          |||
349 GPGSEKYSDDTKYTDGLPAADLI PPLKPRKWIIISADHPYVDVVLFK 398
          |||
235 TEFLQNHCARSEVILEKWKQKKIAEMGPVQLATQK...KAADKVVFLLS 280
          |||
399 AQFLLTACCTEVALDLLEEQAISEAGVMTWGRQKQEMVBESNKIIVLCS 448
          |||
281 NDVNSVCDTCGCKSEGSP.....SENSODLFPLAFNLFCSDLRSQIHL 323
          |||
449 RGTRAKWQALLGR..GAPVRLRCDHGKPVQDLFTAAMNMILPDFKRPFAC 496
          |||
    32 HKYVVVYFREIDTKDDY.NALSVCPKYHLMK...DATAFCAEHLHWKQQVS 370
          |||::|||
497 GTYYVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFPQGR 546
          |||
371 AGKRSQACHDGCCSL*..... 386
          |||
547 MHRVGELSGDNYLRSPPGGRQLRAALDRFDWQRCPDWFEENLYSADDQ 596

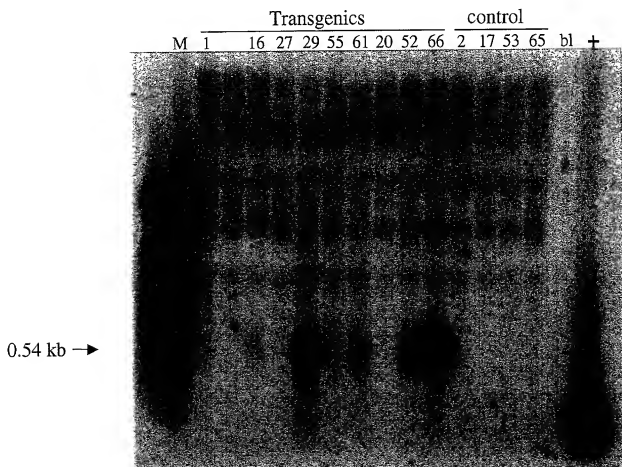
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FIGURE 7
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17
Receptor Like Polypeptides

1	<u>MSLVLLSLAA</u>	<u>LCRS</u>	SAVPREP	TVQCGSETGP	SPEWMLQHD	IPGDLRDLRV
1	<u>MSLVLLSLAA</u>	<u>LCRS</u>	SAVPREP	TVQCGSETGP	SPEWMLQHD	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNVS	W	VLRADASIRL	LKATKICVTG	KSNFQSYSCV
51	EPVTTSVATG	DYSILMNVS	W	VLRADASIRL	LKATKICVTG	KSNFQSYSCV
101	RCNYTEAFQT	QTRPSGGK	--	-----	-----	-----
101	RLECSGAIMA	RCDLNLGSS		DRSASASRAA	GTAGVGHQNW	LIFVVFVEGG
119	-----	-----	-----	WTFS	YIGFPVELNT	VYFIGAHNIP
151	FTVLLVLN	SAQAICLPRLP		KVLGLQWTFS	YIGFPVELNT	VYFIGAHNIP
1				MWTF	YIGFPVELNT	VYFIGAHNIP
143	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
201	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
26	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
193	TVEVNFTTTP	LGNRYMALIQ		HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
251	TVEVNFTTTP	LGNRYMALIQ		HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
76	TVEVNFTTTP	LGNRYMALIQ		HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
243	SEGATVQLTP	YFPTCGSDCI		RHKGTVVLC	QTGVPPFLDN	NKSKPGGWLP
301	SEGATVQLTP	YFPTCGSDCI		RHKGTVVLC	QTGVPPFLDN	NKSKPGGWLP
126	SEGATVQLTP	YFPTCGSDCI		RHKGTVVLC	QTGVPPFLDN	NKSKPGGWLP
293	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>		WRHERIKKTS	FSTTTLLPPI	KVLVVYPSEI
351	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>		WRHERIKKTS	FSTTTLLPPI	KVLVVYPSEI
176	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>		WRHERIKKTS	FSTTTLLPPI	KVLVVYPSEI
343	CFHHTICYFT	EFLQNHCRSE		VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
401	CFHHTICYFT	EFLQNHCRSE		VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
226	CFHHTICYFT	EFLQNHCRSE		VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
393	VFLLSNDVNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
451	VFLLSNDVNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
276	VFLLSNDVNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
443	YVVVYFREID	TKDDYNALSV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
501	YVVVYFREID	TKDDYNALSV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
326	YVVVYFREID	TKDDYNALSV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
493	QACHDGCCSL		*			
551	QACHDGCCSL		*			
376	QACHDGCCSL		*			

Figure 8

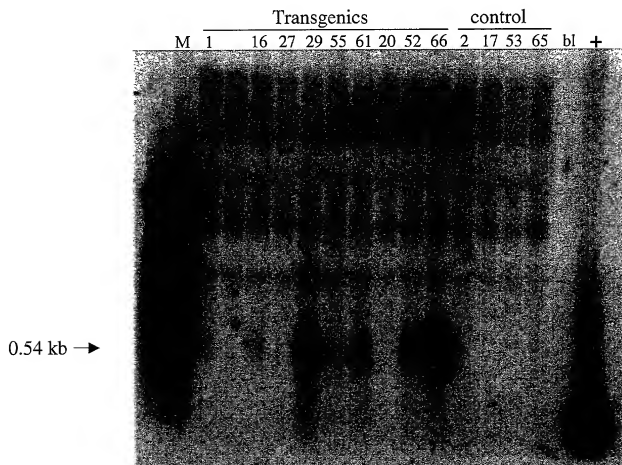
Northern Blot Expression Analysis of TH00-018 Necropsied Transgenic Founders



0010927-031504

Figure 9

Northern Blot Expression Analysis of TH00-018 Necropsied Transgenic Founders



00040927-031604

Figure 10

Non-Transgenics

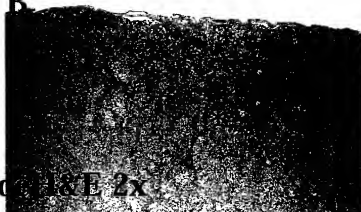
IL-17E Transgenics

A



Lymph Node H&E 2x

B

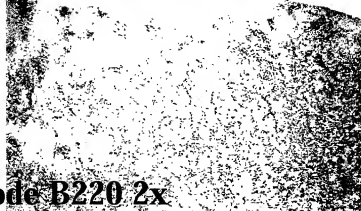


C



Lymph Node B220 2x

D

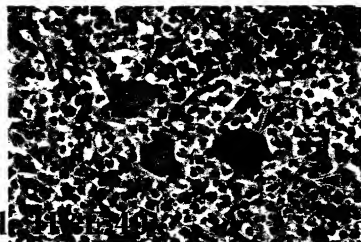
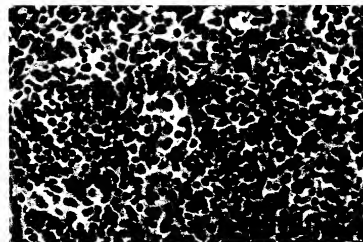
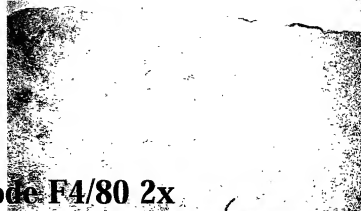


E



Lymph Node F4/80 2x

F



09810927-021501

10/11/01

Figure 11

Non-Transgenics

IL-17E Transgenics

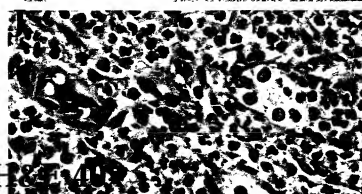
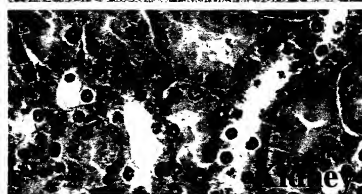
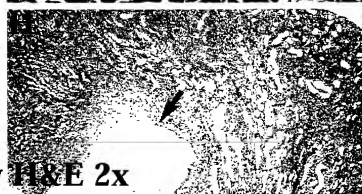
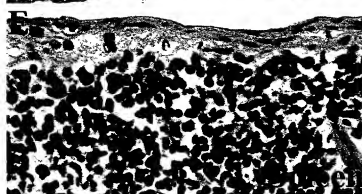
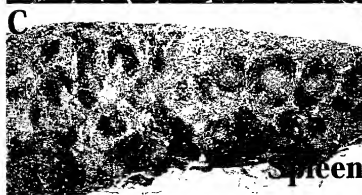
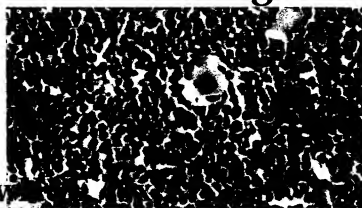
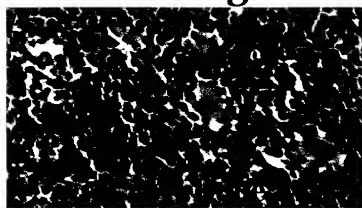
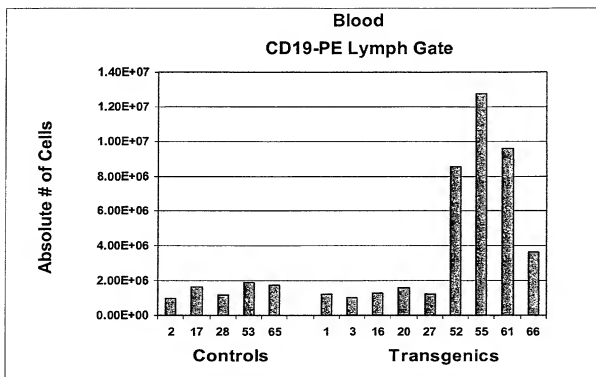


Figure 12



109320-22001860

Figure 13

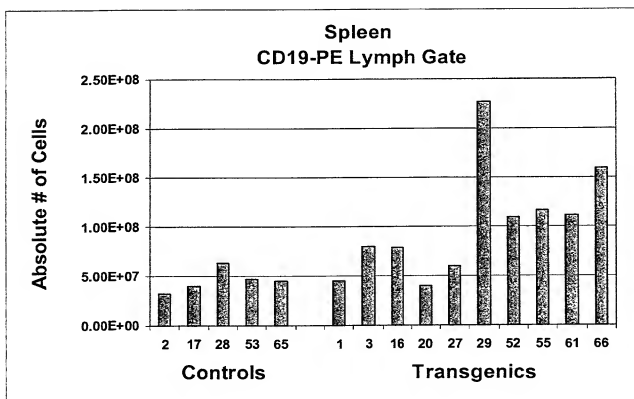
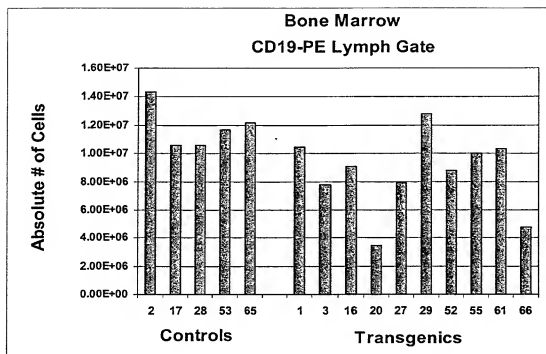


Figure 14



FOSTER: 22001862

Figure 15

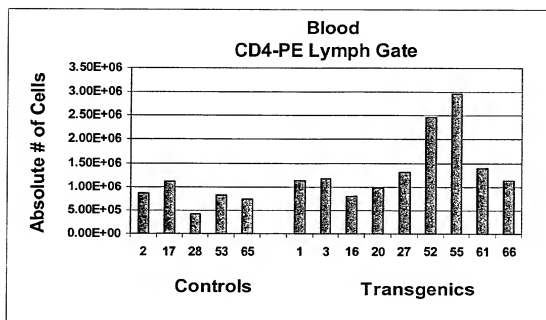


Figure 16

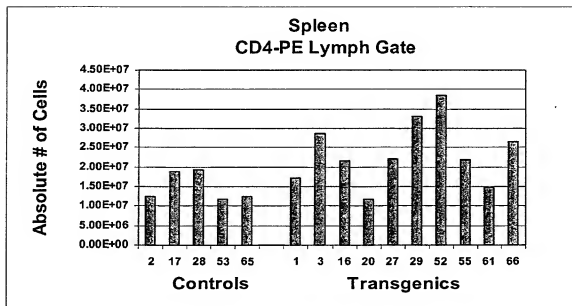


Figure 17

CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

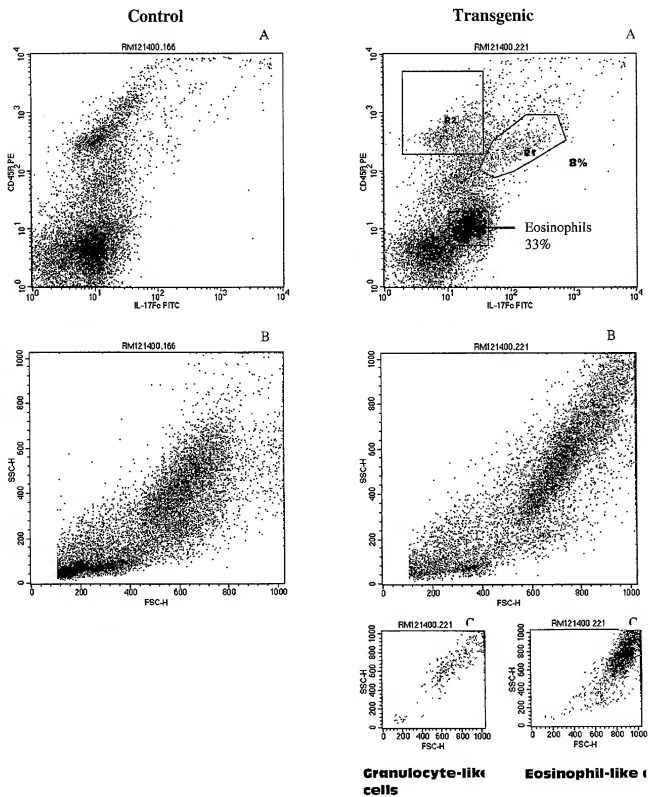
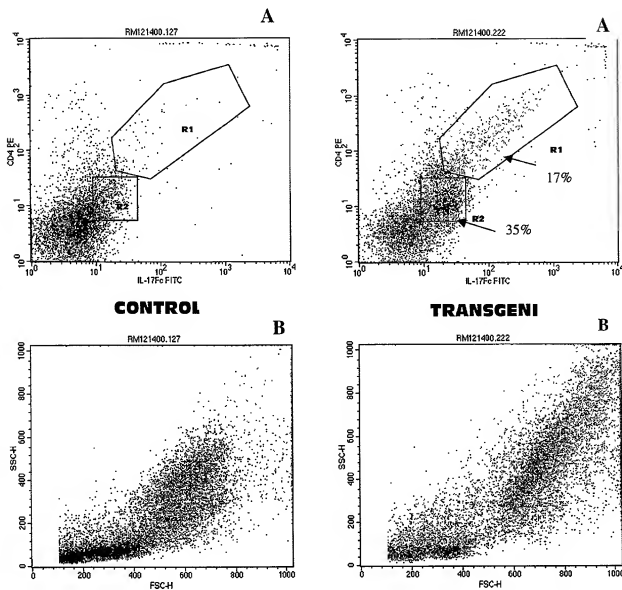


Figure 18

CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW



109120 2201300

Figure 19

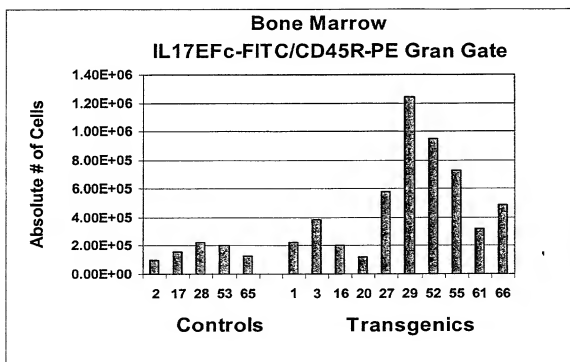


Figure 20

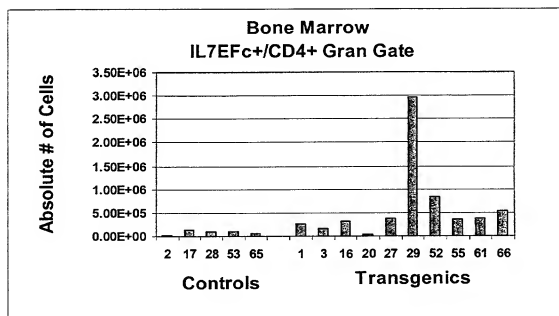
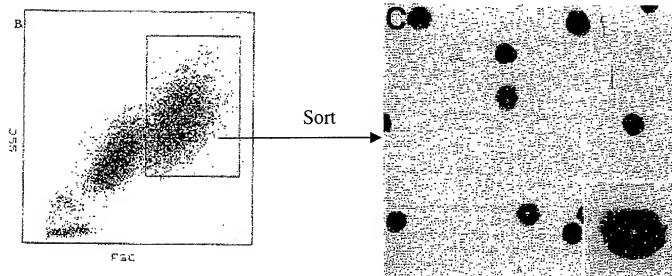


Figure 21

Example of a typical eosinophil Forward vs. Side scatter plot (size vs. granularity). Cells in the gate can be sorted to give a purified population.



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Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

```

1      MSLVLLSLAA LCRSAVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51     EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
101    RCNYTEAFQT QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG
151    PMSMVNFTSP GCLDHIMKYK KKCVKAGSLW DPNITACKKN EETVEVNFTT
201    TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL
251    TPYFPTCGSD CIRHKGTVVL CPQTGVPPFL DNNKSKPGGW LPAAAEPKSC
301    DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
351    PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK
401    CKVSNKALPA PIEKTISKAK GQPREPQVYT LPISRDELTK NQVSLTCLVK
451    GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG
501    NVFSCSVMHE ALHNHYTQKS LSLSPGK*

```

0001007:0260

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1	<u>MSLVLLSLAA</u>	<u>LCRS</u>	AVPREP	TVQCGSETGP	SPEWMLQHD	IPGDLRDLRV
51	EPVTTTSVATG	DYSILMNVS	WVLRADASIRL	LKATKICVTG	KSNFQSYSCV	
101	RLECSGAIMA	RCDLNLLGSS	DRSASASRAA	GTAGVGHQTW	LIFVVVVEGG	
151	FTVLLVLNSS	AQAICLPRLP	KVLGLQWTF	SYIGFPVELNT	VYFIGAHNIP	
201	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE	
251	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPTVGD	
301	SEGATVQLTP	YFPTCGSDCI	RHKGTVVLC	PQTGVVFFPLD	NKSKPGGWLP	
351	<u>AAAEPKSCDK</u>	<u>THTCPPCPAP</u>	<u>ELLGGPSVFL</u>	<u>FPPKPKDTLM</u>	<u>ISRTPEVTCV</u>	
401	<u>VVDVSHEDPE</u>	<u>VKFNWYVDGV</u>	<u>EVHNAKTKPR</u>	<u>EEQYNSTYRV</u>	<u>VSVLTVLHQD</u>	
451	WLNKEYKCK	VSNKALPAPI	EKTISKAKGQ	PREPQVYTL	PSRDELTKNQ	
501	<u>VSLTCLVKGF</u>	<u>YPSDIAVEWE</u>	<u>SNGQPENNYK</u>	<u>TPPVLDSGD</u>	<u>SFFLYSKLTV</u>	
551	<u>DKSRWQQGNV</u>	<u>FSCSVMHEAL</u>	<u>HNHYTQKSLS</u>	<u>LSPGK*</u>		